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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/844,705

DATE: 12/21/2001

TIME: 15:28:27

Input Set : N:\Crf3\RULE60\09844705.txt

Output Set: N:\CRF3\12212001\I844705.raw

ENTERED

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5 <110> APPLICANT: BOSWORTH, BRAD
7 VOGELI, PETER
11 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS TO IDENTIFY SWINE GENETICALLY
13 RESISTANT TO F18 E. COLI ASSOCIATED DISEASES
17 <130> FILE REFERENCE: 21419/90368
19 <140> CURRENT APPLICATION NUMBER: 09/844,705
21 <141> CURRENT FILING DATE: 2001-04-27
23 <150> PRIOR APPLICATION NUMBER: 09/443,766
25 <151> PRIOR FILING DATE: 1999-11-19
29 <160> NUMBER OF SEQ ID NOS: 13
33 <170> SOFTWARE: PatentIn Ver. 2.0
37 <210> SEQ ID NO: 1
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41 <212> TYPE: DNA
43 <213> ORGANISM: Artificial Sequence
47 <220> FEATURE:
49 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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89 <212> TYPE: DNA
91 <213> ORGANISM: Artificial Sequence
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109 <210> SEQ ID NO: 4
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115 <213> ORGANISM: Artificial Sequence
119 <220> FEATURE:
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133 <210> SEQ ID NO: 5
135 <211> LENGTH: 22
137 <212> TYPE: DNA
139 <213> ORGANISM: Artificial Sequence

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143 <220> FEATURE:
145 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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151 tccagagtgg agacaagtct gc 22
157 <210> SEQ ID NO: 6
159 <211> LENGTH: 23
161 <212> TYPE: DNA
163 <213> ORGANISM: Artificial Sequence
167 <220> FEATURE:
169 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
173 <400> SEQUENCE: 6
175 ctgcctgaac gtctatcaag atc 23
181 <210> SEQ ID NO: 7
183 <211> LENGTH: 22
185 <212> TYPE: DNA
187 <213> ORGANISM: Artificial Sequence
191 <220> FEATURE:
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199 agagtttcct catgcccaca gg 22
205 <210> SEQ ID NO: 8
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209 <212> TYPE: DNA
211 <213> ORGANISM: Artificial Sequence
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223 ctgctacagg accaccagca tc 22
229 <210> SEQ ID NO: 9
231 <211> LENGTH: 35
233 <212> TYPE: DNA
235 <213> ORGANISM: Artificial Sequence
239 <220> FEATURE:
241 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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289 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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305 <212> TYPE: DNA
307 <213> ORGANISM: Porcine
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315 <222> LOCATION: (9)..(1103)
319 <400> SEQUENCE: 12
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323 Met Trp Val Pro Ser Arg Arg His Leu Cys Leu Thr Phe Leu
325 1 5 10
329 cta gtc tgt gtt tta gca gca att ttc ttc ctg aac gtc tat caa gac 98
331 Leu Val Cys Val Leu Ala Ala Ile Phe Phe Leu Asn Val Tyr Gln Asp
333 15 20 25 30
337 ctc ttt tac agt ggc tta gac ctg ctg gcc ctg tgt cca gac cat aac 146
339 Leu Phe Tyr Ser Gly Leu Asp Leu Leu Ala Leu Cys Pro Asp His Asn
341 35 40 45
345 gtg gta tca tct ccc gtg gcc ata ttc tgc ctg gcg ggc acg ccg gta 194
347 Val Val Ser Ser Pro Val Ala Ile Phe Cys Leu Ala Gly Thr Pro Val
349 50 55 60
353 cac ccc aac gcc tcc gat tcc tgt ccc aag cat cct gcc tcc ttt tcc 242
355 His Pro Asn Ala Ser Asp Ser Cys Pro Lys His Pro Ala Ser Phe Ser
357 65 70 75
361 ggg acc tgg act att tac ccg gat ggc cgg ttt ggg aac cag atg gga 290
363 Gly Thr Trp Thr Ile Tyr Pro Asp Gly Arg Phe Gly Asn Gln Met Gly
365 80 85 90
369 cag tat gcc acg ctg ctg gcc ctg gcg cag ctc aac ggc cgc cag gcc 338
371 Gln Tyr Ala Thr Leu Leu Ala Leu Ala Gln Leu Asn Gly Arg Gln Ala
373 95 100 105 110
377 ttc atc cag cct gcc atg cac gcc gtc ctg gcc ccc gtg ttc cgc atc 386
379 Phe Ile Gln Pro Ala Met His Ala Val Leu Ala Pro Val Phe Arg Ile
381 115 120 125
385 acg ctg cct gtc ctg gcg ccc gag gta gac agg cac gct cct tgg cgg 434
387 Thr Leu Pro Val Leu Ala Pro Glu Val Asp Arg His Ala Pro Trp Arg
389 130 135 140
393 gag ctg gag ctt cac gac tgg atg tcc gag gat tat gcc cac tta aag 482
395 Glu Leu Glu Leu His Asp Trp Met Ser Glu Asp Tyr Ala His Leu Lys
397 145 150 155
401 gag ccc tgg ctg aag ctc acc ggc ttc ccc tgc tcc tgg acc ttc ttc 530
403 Glu Pro Trp Leu Lys Leu Thr Gly Phe Pro Cys Ser Trp Thr Phe Phe
405 160 165 170
409 cac cac ctc cgg gag cag atc cgc agc gag ttc acc ctg cac gac cac 578
411 His His Leu Arg Glu Gln Ile Arg Ser Glu Phe Thr Leu His Asp His
413 175 180 185 190
417 ctt cgg caa gag gcc cag ggg gta ctg agt cag ttc cgt cta ccc cgc 626
419 Leu Arg Gln Glu Ala Gln Gly Val Leu Ser Gln Phe Arg Leu Pro Arg

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421          195          200          205
425 aca ggg gac cgc ccc agc acc ttc gtg ggg gtc cac gtg cgc cgc ggg 674
427 Thr Gly Asp Arg Pro Ser Thr Phe Val Gly Val His Val Arg Arg Gly
429          210          215          220
433 gac tat ctg cgt gtg atg ccc aag cgc tgg aag ggg gtg gtg ggt gac 722
435 Asp Tyr Leu Arg Val Met Pro Lys Arg Trp Lys Gly Val Val Gly Asp
437          225          230          235
441 ggc cgt tac ctc cag cag gct atg gac tgg ttc cgg gcc cga tac gaa 770
443 Gly Arg Tyr Leu Gln Gln Ala Met Asp Trp Phe Arg Ala Arg Tyr Glu
445          240          245          250
449 gcc ccc gtc ttt gtg gtc acc agc aac ggc atg gag tgg tgc cgg aag 818
451 Ala Pro Val Phe Val Val Thr Ser Asn Gly Met Glu Trp Cys Arg Lys
453 255          260          265          270
457 aac atc gac acc tcc cgg ggg gac gtg atc ttt gct ggc gat ggg cgg 866
459 Asn Ile Asp Thr Ser Arg Gly Asp Val Ile Phe Ala Gly Asp Gly Arg
461          275          280          285
465 gag gcc gcg ccc gcc agg gac ttt gcg ctg ctg gtg cag tgc aac cac 914
467 Glu Ala Ala Pro Ala Arg Asp Phe Ala Leu Leu Val Gln Cys Asn His
469          290          295          300
473 acc atc atg acc att ggc acc ttc ggc ttc tgg gcc gcc tac ctg gct 962
475 Thr Ile Met Thr Ile Gly Thr Phe Gly Phe Trp Ala Ala Tyr Leu Ala
477          305          310          315
481 ggt gga gat acc atc tac ttg gct aac ttc acc ctg ccc act tcc agc 1010
483 Gly Gly Asp Thr Ile Tyr Leu Ala Asn Phe Thr Leu Pro Thr Ser Ser
485          320          325          330
489 ttc ctg aag atc ttt aaa ccc gag gct gcc ttc ctg ccc gag tgg gtg 1058
491 Phe Leu Lys Ile Phe Lys Pro Glu Ala Ala Phe Leu Pro Glu Trp Val
493 335          340          345          350
497 ggc att aat gca gac ttg tct cca ctc cag atg ttg gct ggg cct 1103
499 Gly Ile Asn Ala Asp Leu Ser Pro Leu Gln Met Leu Ala Gly Pro
501          355          360          365
505 tgaaccagcc aggagccttt ctggaatagc ctgggtcaac ccagggccag cgttatgggt 1163
509 ctccggaagc ccgagtaact tccggagatg ctgggtggtcc tgtagcaggc tggacactta 1223
513 ttccaagagt gattctaatt ggctggactc agaggaaacc ctgcag 1269
519 <210> SEQ ID NO: 13
521 <211> LENGTH: 365
523 <212> TYPE: PRT
525 <213> ORGANISM: Porcine
529 <400> SEQUENCE: 13
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533 1 5 10 15
537 Cys Val Leu Ala Ala Ile Phe Phe Leu Asn Val Tyr Gln Asp Leu Phe
539 20 25 30
543 Tyr Ser Gly Leu Asp Leu Leu Ala Leu Cys Pro Asp His Asn Val Val
545 35 40 45
549 Ser Ser Pro Val Ala Ile Phe Cys Leu Ala Gly Thr Pro Val His Pro
551 50 55 60
555 Asn Ala Ser Asp Ser Cys Pro Lys His Pro Ala Ser Phe Ser Gly Thr
557 65 70 75 80

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561 Trp Thr Ile Tyr Pro Asp Gly Arg Phe Gly Asn Gln Met Gly Gln Tyr
563      85      90      95
567 Ala Thr Leu Leu Ala Leu Ala Gln Leu Asn Gly Arg Gln Ala Phe Ile
569      100      105      110
573 Gln Pro Ala Met His Ala Val Leu Ala Pro Val Phe Arg Ile Thr Leu
575      115      120      125
579 Pro Val Leu Ala Pro Glu Val Asp Arg His Ala Pro Trp Arg Glu Leu
581      130      135      140
585 Glu Leu His Asp Trp Met Ser Glu Asp Tyr Ala His Leu Lys Glu Pro
587 145      150      155      160
591 Trp Leu Lys Leu Thr Gly Phe Pro Cys Ser Trp Thr Phe Phe His His
593      165      170      175
597 Leu Arg Glu Gln Ile Arg Ser Glu Phe Thr Leu His Asp His Leu Arg
599      180      185      190
603 Gln Glu Ala Gln Gly Val Leu Ser Gln Phe Arg Leu Pro Arg Thr Gly
605      195      200      205
609 Asp Arg Pro Ser Thr Phe Val Gly Val His Val Arg Arg Gly Asp Tyr
611      210      215      220
615 Leu Arg Val Met Pro Lys Arg Trp Lys Gly Val Val Gly Asp Gly Arg
617 225      230      235      240
621 Tyr Leu Gln Gln Ala Met Asp Trp Phe Arg Ala Arg Tyr Glu Ala Pro
623      245      250      255
627 Val Phe Val Val Thr Ser Asn Gly Met Glu Trp Cys Arg Lys Asn Ile
629      260      265      270
633 Asp Thr Ser Arg Gly Asp Val Ile Phe Ala Gly Asp Gly Arg Glu Ala
635      275      280      285
639 Ala Pro Ala Arg Asp Phe Ala Leu Leu Val Gln Cys Asn His Thr Ile
641      290      295      300
645 Met Thr Ile Gly Thr Phe Gly Phe Trp Ala Ala Tyr Leu Ala Gly Gly
647 305      310      315      320
651 Asp Thr Ile Tyr Leu Ala Asn Phe Thr Leu Pro Thr Ser Ser Phe Leu
653      325      330      335
657 Lys Ile Phe Lys Pro Glu Ala Ala Phe Leu Pro Glu Trp Val Gly Ile
659      340      345      350
663 Asn Ala Asp Leu Ser Pro Leu Gln Met Leu Ala Gly Pro
665      355      360      365

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